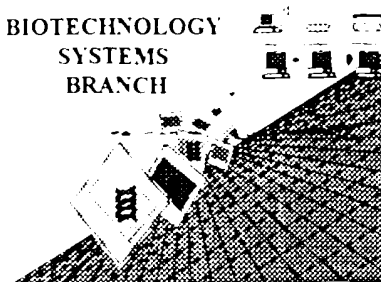


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



11/9
Linda
10/6/00

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/435,257

Source: 1632

Date Processed by STIC: 9/26/2000

RECEIVED

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY
EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT
COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY
or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,
WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/435,257

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.
- 12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk

US 409 435,257

Input File: A:\385_a.dmp
Output File: N:\CPH\9-02620001\1435257.rdw

see p. 5, too

Does Not Comply
Corrected Diskette Needed

[illegible]

→ these numeric identifiers are
mandatory whenever
CR137 response is
Artificial Sequence
(see item 12
on Eva summary
sheet)

RAW SEQUENCE LISTING

PATENT ABSTRACTS IN U.S. 59, 435, 257

File Name: A:\385 a.app

File Name: N:\CRF3\09262000\1435257.r4w

[illegible]

RAW SEQUENCE LISTING
 Patent 1435257 US, 09, 435,257

Input File: A:\485 a.app
 Input Seq: N:\CRE\3092b2000\1435257.raw

```

141 >141< SEQ ID NO: 11
142 >141< LENGTH: 11
143 >141< TYPE: DNA
144 >141< ORGANISM: Artificial Sequence
145 >141< FEATURE:
146 >141< OTHER INFORMATION: Description of Artificial Sequence: synthetic
147 >141< oligonucleotide
148 >141< SEQUENCE: 11
149 ttaatataga tctgagcctt cacttctat cctctcttt cttctgacc aatataaa
150 >141< SEQ ID NO: 12
151 >141< LENGTH: 11
152 >141< TYPE: DNA
153 >141< ORGANISM: Artificial Sequence
154 >141< FEATURE:
155 >141< OTHER INFORMATION: Description of Artificial Sequence: synthetic
156 >141< oligonucleotide
157 >141< SEQUENCE: 12
158 gatttatat gaggcttata tatctctaa cagagctaa accagaaca gttctgaa
159 >141< SEQ ID NO: 13
160 >141< LENGTH: 18
161 >141< TYPE: DNA
162 >141< ORGANISM: Artificial Sequence
163 >141< FEATURE:
164 >141< OTHER INFORMATION: Description of Artificial Sequence: synthetic
165 >141< oligonucleotide
166 >141< SEQUENCE: 13
167 gattgagaa tctatctta gttctctat atttatatg gattttaa cagagaa
168 >141< SEQ ID NO: 14
169 >141< LENGTH: 18
170 >141< TYPE: DNA
171 >141< ORGANISM: Artificial Sequence
172 >141< FEATURE:
173 >141< OTHER INFORMATION: Description of Artificial Sequence: synthetic
174 >141< oligonucleotide
175 >141< SEQUENCE: 14
176 gattgagaa tctatctta gttctctat atttatatg gattttaa cagagaa
177 >141< SEQ ID NO: 15
178 >141< LENGTH: 18
179 >141< TYPE: DNA
180 >141< ORGANISM: Artificial Sequence
181 >141< FEATURE:
182 >141< OTHER INFORMATION: Description of Artificial Sequence: synthetic
183 >141< oligonucleotide
184 >141< SEQUENCE: 15
185 gattgagaa tctatctta gttctctat atttatatg gattttaa cagagaa
186 >141< SEQ ID NO: 16

```

PAW SEQUENCE LISTING

US, 69, 435, 257

10	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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A:\385 a .app

NR00013909252000\1435237.14w

RAW SEQUENCE LISTING

SS 435.257

Figure 1 illustrates the experimental design. It shows two scenarios: (a) 'No change in the number of subjects' and (b) 'Change in the number of subjects'. In (a), a group of 10 subjects is divided into two groups of 5, each receiving a different treatment (T1 and T2), and then compared. In (b), a group of 10 subjects is divided into two groups of 5, each receiving a different treatment (T1 and T2), and then compared. The results are then compared to a control group of 10 subjects.

A:\385 a.app

N:\CRE3\09252000\1435257.raw

```

178     SEQ ID NO : 1
179     LENGTH : 6
180     TYPE : DNA
181     ORGANISM : Artificial Sequence
182     OTHER INFORMATION : Description of Artificial Sequence: Coding Region
183     ORIGIN
184     ATGATGGAGCTGGTGTACCGAAGAATAAGCAAGTTGAAGTGAAATTTCAGTGCCTC
185     C
186     SEQ ID NO : 2
187     LENGTH : 12
188     TYPE : DNA
189     ORGANISM : Artificial Sequence
190     OTHER INFORMATION : Description of Artificial Sequence: Coding Region
191     ORIGIN
192     GATGGAGCTGGTGTACCGAAGAATAAGCAAGTTGAAGTGAAATTTCAGTGCCTC
193     C
194     SEQ ID NO : 3
195     LENGTH : 12
196     TYPE : DNA
197     ORGANISM : Artificial Sequence
198     OTHER INFORMATION : Description of Artificial Sequence: Coding Region
199     ORIGIN
200     GATGGAGCTGGTGTACCGAAGAATAAGCAAGTTGAAGTGAAATTTCAGTGCCTC
201     C
202     SEQ ID NO : 4
203     LENGTH : 12
204     TYPE : DNA
205     ORGANISM : Artificial Sequence
206     OTHER INFORMATION : Description of Artificial Sequence: Coding Region
207     ORIGIN
208     GATGGAGCTGGTGTACCGAAGAATAAGCAAGTTGAAGTGAAATTTCAGTGCCTC
209     C

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

US, 09,435,257

A:\385 a.app

N:\CRF3\09262000\1435257.1aw

DATE	TIME	LOCATION	DESCRIPTION	AMOUNT	CHECK NO.	DEBIT	CREDIT	BALANCE
1998-01-01	12:00	Home	Initial deposit	1000.00				1000.00
1998-01-05	14:30	Bank	Withdrawal	50.00	101	50.00		950.00
1998-01-10	09:00	Home	Deposit	200.00			200.00	1150.00
1998-01-15	16:00	Bank	Withdrawal	75.00	102	75.00		1075.00
1998-01-20	11:00	Home	Deposit	150.00			150.00	1225.00
1998-01-25	13:00	Bank	Withdrawal	30.00	103	30.00		1195.00
1998-01-30	10:00	Home	Deposit	100.00			100.00	1295.00
1998-02-05	15:00	Bank	Withdrawal	60.00	104	60.00		1235.00
1998-02-10	08:00	Home	Deposit	250.00			250.00	1485.00
1998-02-15	17:00	Bank	Withdrawal	40.00	105	40.00		1445.00
1998-02-20	12:00	Home	Deposit	180.00			180.00	1625.00
1998-02-25	14:00	Bank	Withdrawal	20.00	106	20.00		1605.00
1998-03-01	09:00	Home	Deposit	120.00			120.00	1725.00